OIPE

RAW SEQUENCE LISTING   DATE: 01/15/2002
PATENT APPLICATION: US/10/025,145   TIME: 18:55:54

Input Set : A:\18414seq.txt
Output Set: N:\CRF3\01152002\J025145.raw

Does Not Comply
Corrected Diskette Needed

```
  3 <110> APPLICANT: Croteau, Rodney B
  4         Bohlmann, Joerg
  5         Steele, Christopher L
  6         Phillips, Michael A
  8 <120> TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
 10 <130> FILE REFERENCE: WSUR18414
 12 <140> CURRENT APPLICATION NUMBER: US/10/025,145
 13 <141> CURRENT FILING DATE: 2001-12-19
 15 <150> PRIOR APPLICATION NUMBER: 09/360,545
 16 <151> PRIOR FILING DATE: 1999-07-26
 18 <150> PRIOR APPLICATION NUMBER: 60/052,249
 19 <151> PRIOR FILING DATE: 1997-07-11
 21 <150> PRIOR APPLICATION NUMBER: PCT/US98/14528
 22 <151> PRIOR FILING DATE: 1998-07-10
 24 <160> NUMBER OF SEQ ID NOS: 107
 26 <170> SOFTWARE: PatentIn Ver. 2.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 2196
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Abies grandis
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (69)..(1952)
 36 <223> OTHER INFORMATION: Clone AG2.2 encoding myrcene synthase
 38 <400> SEQUENCE: 1
 39 tgccggcacg aggttatctt gagcttcctc catataggcc aacacatatc atatcaaagg  60
 41 gagcaaga atg gct ctg gtt tct atc tca ccg ttg gct tcg aaa tct tgc  110
 42          Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys
 43            1               5                  10
 45 ctg cgc aag tcg ttg atc agt tca att cat gaa cat aag cct ccc tat  158
 46 Leu Arg Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr
 47  15              20                  25                  30
 49 aga aca atc cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg  206
 50 Arg Thr Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr
 51              35                  40                  45
 53 cct tcc atg agc atc agt ttg gcc acc gct gca cct gat gat ggt gta  254
 54 Pro Ser Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val
 55          50                  55                  60
 57 caa aga cgc ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc  302
 58 Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe
 59          65                  70                  75
 61 ata cag tct cta tca acg cct tat ggg gaa ccc tct tac cag gaa cgt  350
 62 Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg
 63      80                  85                  90
 65 gct gag aga tta att gtg gag gta aag aag ata ttc aat tca atg tac  398
 66 Ala Glu Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr
 67  95                  100                 105                 110
```

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```
69  ctg gat gat gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc   446
70  Leu Asp Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg
71                  115                 120                 125

73  ctt tgg ata gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc   494
74  Leu Trp Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe
75                  130                 135                 140

77  aag aac gag ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag   542
78  Lys Asn Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu
79              145                 150                 155

81  gaa aac ggc att gga tgt ggg aga gac agt att gtt act gat ctc aac   590
82  Glu Asn Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn
83          160                 165                 170

85  tca act gcg ttg ggg ttt cga act ctt cga tta cac ggg tac act gta   638
86  Ser Thr Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val
87  175                 180                 185                 190

89  tct cca gag gtt tta aaa gct ttt caa gat caa aat gga cag ttt gta   686
90  Ser Pro Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val
91                  195                 200                 205

93  tgc tcc ccc ggt cag aca gag ggt gag atc aga agc gtt ctt aac tta   734
94  Cys Ser Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu
95              210                 215                 220

97  tat cgg gct tcc ctc att gcc ttc cct ggt gag aaa gtt atg gaa gaa   782
98  Tyr Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu
99          225                 230                 235

101 gct gaa atc ttc tcc aca aga tat ttg aaa gaa gct cta caa aag att   830
102 Ala Glu Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile
103     240                 245                 250

105 cca gtc tcc gct ctt tca caa gag ata aag ttt gtt atg gaa tat ggc   878
106 Pro Val Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly
107 255                 260                 265                 270

109 tgg cac aca aat ttg cca aga ttg gaa gca aga aat tac ata gac aca   926
110 Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr
111                 275                 280                 285

113 ctt gag aaa gac acc agt gca tgg ctc aat aaa aat gct ggg aag aag   974
114 Leu Glu Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys
115             290                 295                 300

117 ctt tta gaa ctt gca aaa ttg gag ttc aat ata ttt aac tcc tta caa   1022
118 Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln
119             305                 310                 315

121 caa aag gaa tta caa tat ctt ttg aga tgg tgg aaa gag tcg gat ttg   1070
122 Gln Lys Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu
123     320                 325                 330

125 cct aaa ttg aca ttt gct cgg cat cgt cat gtg gaa ttc tac act ttg   1118
126 Pro Lys Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu
127 335                 340                 345                 350

129 gcc tct tgt att gcc att gac cca aaa cat tct gca ttc aga cta ggc   1166
130 Ala Ser Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly
131             355                 360                 365

133 ttc gcc aaa atg tgt cat ctt gtc aca gtt ttg gac gat att tac gac   1214
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```
134 Phe Ala Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp
135             370             375             380
137 act ttt gga acg att gac gag ctt gaa ctc ttc aca tct gca att aag   1262
138 Thr Phe Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys
139         385             390             395
141 aga tgg aat tca tca gag ata gaa cac ctt cca gaa tat atg aaa tgt   1310
142 Arg Trp Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys
143     400             405             410
145 gtg tac atg gtc gtg ttt gaa act gta aat gaa ctg aca cga gag gcg   1358
146 Val Tyr Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala
147 415             420             425             430
149 gag aag act caa ggg aga aac act ctc aac tat gtt cga aag gct tgg   1406
150 Glu Lys Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp
151             435             440             445
153 gag gct tat ttt gat tca tat atg gaa gaa gca aaa tgg atc tct aat   1454
154 Glu Ala Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn
155         450             455             460
157 ggt tat ctg cca atg ttt gaa gag tac cat gag aat ggg aaa gtg agc   1502
158 Gly Tyr Leu Pro Met Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser
159         465             470             475
161 tct gca tat cgc gta gca aca ttg caa ccc atc ctc act ttg aat gca   1550
162 Ser Ala Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala
163     480             485             490
165 tgg ctt cct gat tac atc ttg aag gga att gat ttt cca tcc agg ttc   1598
166 Trp Leu Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe
167 495             500             505             510
169 aat gat ttg gca tcg tcc ttc ctt cgg cta cga ggt gac aca cgc tgc   1646
170 Asn Asp Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys
171             515             520             525
173 tac aag gcc gat agg gat cgt ggt gaa gaa gct tcg tgt ata tca tgt   1694
174 Tyr Lys Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys
175             530             535             540
177 tat atg aaa gac aat cct gga tca acc gaa gaa gat gcc ctc aat cat   1742
178 Tyr Met Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His
179         545             550             555
181 atc aat gcc atg gtc aat gac ata atc aaa gaa tta aat tgg gaa ctt   1790
182 Ile Asn Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu
183     560             565             570
185 cta aga tcc aac gac aat att cca atg ctg gcc aag aaa cat gct ttt   1838
186 Leu Arg Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe
187 575             580             585             590
189 gac ata aca aga gct ctc cac cat ctc tac ata tat cga gat ggc ttt   1886
190 Asp Ile Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe
191             595             600             605
193 agt gtt gcc aac aag gaa aca aaa aaa ttg gtt atg gaa aca ctc ctt   1934
194 Ser Val Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu
195             610             615             620
197 gaa tct atg ctt ttt taa ctataaccat atccataata ataagctcat          1982
198 Glu Ser Met Leu Phe
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199           625
201 aatgctaaat tattggcctt atgacatagt ttatgtatgt acttgtgtga attcaatcat 2042
203 atcgtgtggg tatgattaaa aagctagagc ttactaggtt agtaacatgg tgataaaagt 2102
205 tataaaatgt gagttataga gatacccatg ttgaataatg aattacaaaa agagaaattt 2162
207 atgtagaata agattggaag cttttcaatt gttt                            2196
210 <210> SEQ ID NO: 2
211 <211> LENGTH: 627
212 <212> TYPE: PRT
213 <213> ORGANISM: Abies grandis
215 <400> SEQUENCE: 2
216 Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg
217  1               5                  10                 15
219 Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr
220             20                  25                 30
222 Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser
223         35                  40                 45
225 Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg
226     50                  55                 60
228 Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Phe Ile Gln
229  65              70                 75                 80
231 Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu
232             85                  90                 95
234 Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp
235             100                 105                110
237 Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp
238         115                 120                 125
240 Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
241     130                 135                 140
243 Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn
244 145                 150                 155                160
246 Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr
247             165                 170                175
249 Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro
250         180                 185                190
252 Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser
253         195                 200                 205
255 Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg
256     210                 215                 220
258 Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
259 225                 230                 235                240
261 Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val
262             245                 250                255
264 Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His
265         260                 265                 270
267 Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu
268         275                 280                 285
270 Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu
271     290                 295                 300
273 Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys
```

```
274 305                     310                 315                 320
276 Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys
277                 325                 330                 335
279 Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser
280                 340                 345                 350
282 Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala
283             355                 360                 365
285 Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe
286     370                 375                 380
288 Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp
289 385                 390                 395                 400
291 Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr
292                 405                 410                 415
294 Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys
295                 420                 425                 430
297 Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala
298             435                 440                 445
300 Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr
301     450                 455                 460
303 Leu Pro Met Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala
304 465                 470                 475                 480
306 Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu
307             485                 490                 495
309 Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp
310             500                 505                 510
312 Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys
313             515                 520                 525
315 Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met
316     530                 535                 540
318 Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn
319 545                 550                 555                 560
321 Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg
322             565                 570                 575
324 Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile
325             580                 585                 590
327 Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val
328     595                 600                 605
330 Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser
331     610                 615                 620
333 Met Leu Phe
334 625
337 <210> SEQ ID NO: 3
338 <211> LENGTH: 2018
339 <212> TYPE: DNA
340 <213> ORGANISM: Abies grandis
342 <220> FEATURE:
343 <221> NAME/KEY: CDS
344 <222> LOCATION: (6)..(1892)
345 <223> OTHER INFORMATION: Clone AG3.18 encoding pinene synthase
```

```
<210>          11
<211>         108
<212>     DNA
<213>     Artificial Sequence
<220>
<223>
```

→ see item 11 on Euro Summary sheet

```
<400>         11
          gatgatgggt ttgatgcgca cggaacccta gatgaattga agctattcac tgaggctgtg 60
          agaagatggg acctctcctt tacagacaac ttccccgatt acatgaaa              108
```

FYI

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

<210>   25
<211> .   8
<212>   · PRT
<213>   : Artificial Sequence
<220> ·
<223>   : Description of Artificial Sequence: conserved
         amino acid motif on which the sequence of Primer D
         was based, wherein Xaa at position number 3 represents Thr or Ile, Xaa at
         position number 4 represents Ile or Tyr or Phe, Xaa at position number 6
<2207 ←——————
         ←⟨2237⟩represents Ala or Val and Xaa at position number 8 represents Ala or Gly

Per 1.823 of Sequence Rules, 4 lines maximum for ⟨2237⟩ response. Insert another ⟨2207⟩ after 4th line and insert a ⟨2237⟩ on 5th line.

IMPORTANT: The types of errors shown exist throughout
                     the Sequence Listing. Please check subsequent
                     sequences for similar errors.

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```
L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:983 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1003 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1023 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1031 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1031 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1077 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1949 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1969 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1989 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2027 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2036 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:2058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:2072 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2081 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:2102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:2609 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:45
L:2609 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:45
L:2609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:2623 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2626 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:2626 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:2626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:2672 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2689 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2692 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:50
L:2692 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:50
L:2692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:2706 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2709 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:51
L:2709 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:2709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:2723 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2726 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:52
L:2726 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:52
L:2726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:2740 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2743 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:53
L:2743 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:53
L:2743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:2786 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:56
L:2786 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:56
L:2786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
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